

SEQUENCE LISTING

<110> Merck Patent GmbH

<120> Acute neuronal induced binding protein (ANIC-BP-1B)

<130> ANICBP1BIDWS

<140>

<141>

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 1053

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1053)

<400> 1

atg ccg ttc ccg ttt ggg aag tct cac aaa tct cca gca gac att gtg 48
Met Pro Phe Pro Phe Gly Lys Ser His Lys Ser Pro Ala Asp Ile Val
1 5 10 15

aag aat ctg aag gag agc atg gct gtt ctg gaa aag caa gac att tct 96
Lys Asn Leu Lys Glu Ser Met Ala Val Leu Glu Lys Gln Asp Ile Ser
20 25 30

gat aaa aaa gca gaa aag gct aca gaa gaa gtt tcc aaa aat ctg gtt 144
Asp Lys Lys Ala Glu Lys Ala Thr Glu Glu Val Ser Lys Asn Leu Val
35 40 45

gcc atg aaa gaa att ctg tat ggc aca aat gaa aaa gag cct cag aca 192
Ala Met Lys Glu Ile Leu Tyr Gly Thr Asn Glu Lys Glu Pro Gln Thr
50 55 60

gaa gca gta gct caa ctt gct caa gaa ctc tat aat agt ggg ctc ctt 240
Glu Ala Val Ala Gln Leu Ala Gln Glu Leu Tyr Asn Ser Gly Leu Leu
65 70 75 80

agc acc ctg gta gct gat tta cag ctc att gac ttt gag ggc aaa aaa 288
Ser Thr Leu Val Ala Asp Leu Gln Leu Ile Asp Phe Glu Gly Lys Lys
85 90 95

gac gtg gct caa att ttc aac aat att ctc aga aga caa att ggt acg 336
Asp Val Ala Gln Ile Phe Asn Asn Ile Leu Arg Arg Gln Ile Gly Thr
100 105 110

aga act cct act gtt gaa tac atc tgc acc caa cag aat att ttg ttc		384	
Arg Thr Pro Thr Val Glu Tyr Ile Cys Thr Gln Gln Asn Ile Leu Phe			
115	120	125	
atg tta ttg aaa ggg tat gaa tct cca gaa ata gct cta aat tgt gga		432	
Met Leu Leu Lys Gly Tyr Glu Ser Pro Glu Ile Ala Leu Asn Cys Gly			
130	135	140	
ata atg tta aga gaa tgc atc aga cat gaa cca ctt gca aaa atc att		480	
Ile Met Leu Arg Glu Cys Ile Arg His Glu Pro Leu Ala Lys Ile Ile			
145	150	155	160
ttg tgg tcg gaa cag ttt tat gat ttc ttc aga tat gtc gaa atg tca		528	
Leu Trp Ser Glu Gln Phe Tyr Asp Phe Phe Arg Tyr Val Glu Met Ser			
165	170	175	
aca ttt gac ata gct tca gat gca ttt gcc aca ttc aag gat tta ctt		576	
Thr Phe Asp Ile Ala Ser Asp Ala Phe Ala Thr Phe Lys Asp Leu Leu			
180	185	190	
aca aga cat aaa ttg ctc agt gca gaa ttt ttg gaa cag cat tat gat		624	
Thr Arg His Lys Leu Leu Ser Ala Glu Phe Leu Glu Gln His Tyr Asp			
195	200	205	
aga ttt ttc agt gaa tat gag aag tta ctt cat tca gaa aat tat gtg		672	
Arg Phe Phe Ser Glu Tyr Glu Lys Leu Leu His Ser Glu Asn Tyr Val			
210	215	220	
aca aaa aga cag tca ctg aag ctt ctc ggt gaa cta cta cta gat aga		720	
Thr Lys Arg Gln Ser Leu Lys Leu Leu Gly Glu Leu Leu Leu Asp Arg			
225	230	235	240
cac aac ttc aca att atg aca aaa tac atc agt aaa cct gag aac ctc		768	
His Asn Phe Thr Ile Met Thr Lys Tyr Ile Ser Lys Pro Glu Asn Leu			
245	250	255	
aaa tta atg atg aac ctg ctg cga gac aaa agt cgc aac atc cag ttt		816	
Lys Leu Met Met Asn Leu Leu Arg Asp Lys Ser Arg Asn Ile Gln Phe			
260	265	270	
gag gcc ttt cac gtt ttt aag gtg ttt gta gcc aat cct aac aag acg		864	
Glu Ala Phe His Val Phe Lys Val Phe Val Ala Asn Pro Asn Lys Thr			
275	280	285	
cag ccc atc cta gac atc ctc ctc aag aac cag gcc aaa ctc ata gag		912	
Gln Pro Ile Leu Asp Ile Leu Leu Lys Asn Gln Ala Lys Leu Ile Glu			
290	295	300	
ttc ctc agc aag ttt cag aac gac agg acg gat tgt atg agc agt tcc		960	
Phe Leu Ser Lys Phe Gln Asn Asp Arg Thr Asp Cys Met Ser Ser Ser			
305	310	315	320
gta ccg acg acg aat tcc cggt gtc gat tta cgc gtt aaa ccg cggt acg		1008	
Val Pro Thr Thr Asn Ser Arg Val Asp Leu Arg Val Lys Pro Arg Thr			

325

330

335

cgt ggg atc agg gat ttg aag aga cca gct cag caa gaa gct taa	1053
Arg Gly Ile Arg Asp Leu Lys Arg Pro Ala Gln Gln Glu Ala	
340	345
	350

<210> 2
 <211> 350
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Pro Phe Pro Phe Gly Lys Ser His Lys Ser Pro Ala Asp Ile Val			
1	5	10	15
Lys Asn Leu Lys Glu Ser Met Ala Val Leu Glu Lys Gln Asp Ile Ser			
20	25	30	
Asp Lys Lys Ala Glu Lys Ala Thr Glu Glu Val Ser Lys Asn Leu Val			
35	40	45	
Ala Met Lys Glu Ile Leu Tyr Gly Thr Asn Glu Lys Glu Pro Gln Thr			
50	55	60	
Glu Ala Val Ala Gln Leu Ala Gln Glu Leu Tyr Asn Ser Gly Leu Leu			
65	70	75	80
Ser Thr Leu Val Ala Asp Leu Gln Leu Ile Asp Phe Glu Gly Lys Lys			
85	90	95	
Asp Val Ala Gln Ile Phe Asn Asn Ile Leu Arg Arg Gln Ile Gly Thr			
100	105	110	
Arg Thr Pro Thr Val Glu Tyr Ile Cys Thr Gln Gln Asn Ile Leu Phe			
115	120	125	
Met Leu Leu Lys Gly Tyr Glu Ser Pro Glu Ile Ala Leu Asn Cys Gly			
130	135	140	
Ile Met Leu Arg Glu Cys Ile Arg His Glu Pro Leu Ala Lys Ile Ile			
145	150	155	160
Leu Trp Ser Glu Gln Phe Tyr Asp Phe Arg Tyr Val Glu Met Ser			
165	170	175	
Thr Phe Asp Ile Ala Ser Asp Ala Phe Ala Thr Phe Lys Asp Leu Leu			
180	185	190	
Thr Arg His Lys Leu Leu Ser Ala Glu Phe Leu Glu Gln His Tyr Asp			
195	200	205	
Arg Phe Phe Ser Glu Tyr Glu Lys Leu Leu His Ser Glu Asn Tyr Val			
210	215	220	
Thr Lys Arg Gln Ser Leu Lys Leu Leu Gly Glu Leu Leu Leu Asp Arg			
225	230	235	240
His Asn Phe Thr Ile Met Thr Lys Tyr Ile Ser Lys Pro Glu Asn Leu			
245	250	255	
Lys Leu Met Met Asn Leu Leu Arg Asp Lys Ser Arg Asn Ile Gln Phe			
260	265	270	
Glu Ala Phe His Val Phe Lys Val Phe Val Ala Asn Pro Asn Lys Thr			
275	280	285	
Gln Pro Ile Leu Asp Ile Leu Leu Lys Asn Gln Ala Lys Leu Ile Glu			
290	295	300	
Phe Leu Ser Lys Phe Gln Asn Asp Arg Thr Asp Cys Met Ser Ser Ser			
305	310	315	320
Val Pro Thr Thr Asn Ser Arg Val Asp Leu Arg Val Lys Pro Arg Thr			

325

330

335

Arg Gly Ile Arg Asp Leu Lys Arg Pro Ala Gln Gln Glu Ala

340

345

350